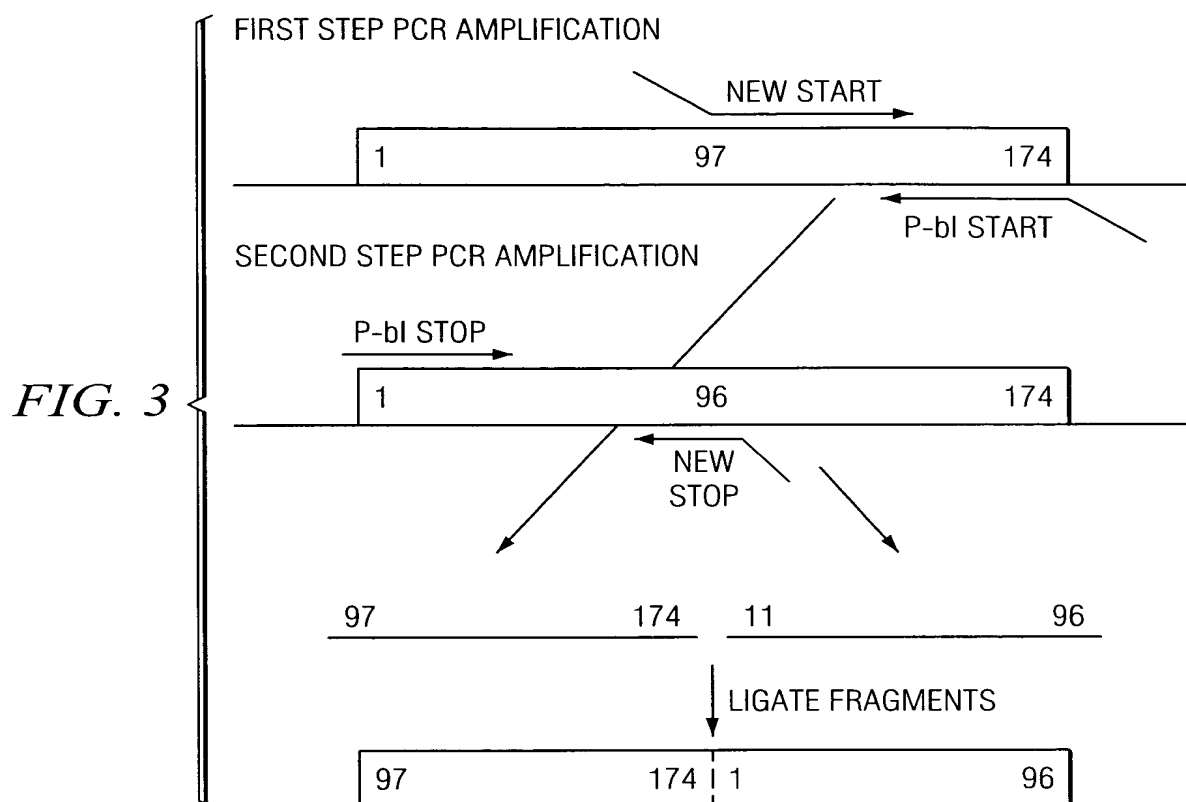


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I. CONSTRUCT TANDEMLY-DUPICATED TEMPLATE



II. PCR-AMPLIFY TANDEMLY-DUPICATED TEMPLATE

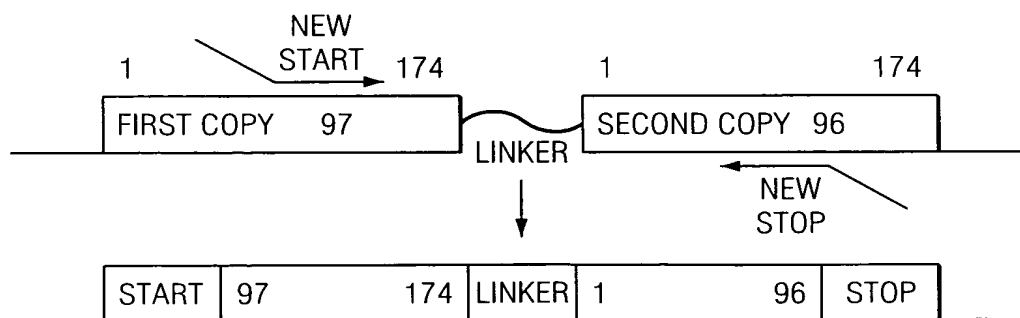


FIG. 4

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```

  ACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGT
1-----+-----+-----+-----+-----+-----+-----+ 60
  TGGGTCTCTGACGAGGAAGGTTGTGTCGGGGTAGAGGAGGCTGAAGCGACAGTTTTAGGCA

  ThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArg
  GAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGAC
61-----+-----+-----+-----+-----+-----+-----+ 120
  CTCGACAGACTGATGGACGAAGTTCTAATGGGTCAGTGGCACCGGAGGTTGGACGTCCTG

  GluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAsp
  GAGGAGCTCTGCGGGGGCCTCTGGCGGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTC
121-----+-----+-----+-----+-----+-----+-----+ 180
  CTCCTCGAGACGCCCCCGGAGACCGCCGACCAGGACCGTGTGCGGACCTACCTCGCCGAG

  GluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeu
  AAGACTGTGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGGAGATACAC
181-----+-----+-----+-----+-----+-----+-----+ 240
  TTCTGACAGCGACCCAGGTTCTACGTTCCGAACGACCTCGCGCACTTGTGCCTCTATGTG

  LysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHis
  TTTGTCACCAAATGTGCCTTTCAGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAAC
241-----+-----+-----+-----+-----+-----+-----+ 300
  AAACAGTGGTTTACACGGAAAGTCGGGGGGGGGTGACAGAAGCGAAGCAGGTCTGGTTG

  PheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsn
  ATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACT
301-----+-----+-----+-----+-----+-----+-----+ 360
  TAGAGGGCGGAGGACGTCCTCTGGAGGCTCGTCGACCACCGCGACTTCGGGACCTAGTGA

  IleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThr
  CGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTACGCCCGACTCCTCAACCCTGCCA
361-----+-----+-----+-----+-----+-----+-----+ 420
  GCGGTCTTGAAGAGGGCCACGGACCTCGACGTCACAGTCGGGCTGAGGAGTTGGGACGGT

  ArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuPro
  CCCCCATGGAGTCCCCGGCCCCCTGGAGGCCACAGCCCCGACAGCCCCGACCCCCCTCTG
421-----+-----+-----+-----+-----+-----+-----+ 480
  GGGGGTACCTCAGGGGCCGGGGACCTCCGGTGTGCGGGCTGTGCGGGCGTCGGGGGAGAC

  ProProTrpSerProArgProLeuGluAlaThrAlaProThrAlaProGlnProProLeu

```

FIG. 5a

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```

CTCCTCCTACTGCTGCTGCCCGTGGGCCTCCTGCTGCTGGCCGCTGCCTGGTGCCTGCAC
481 -----+-----+-----+-----+-----+-----+-----+ 540
GAGGAGGATGACGACGACGGGCACCCGGAGGACGACGACCGGCGACGGACCACGGACGTG

LeuLeuLeuLeuLeuLeuProValGlyLeuLeuLeuLeuAlaAlaAlaTrpCysLeuHis

TGGCAGAGGACGCGGGCGGAGGACACCCCGCCCTGGGGAGCAGGTGCCCCCGTCCCCAGT
541 -----+-----+-----+-----+-----+-----+-----+ 600
ACCGTCTCCTGCGCCGCCTCCTGTGGGGCGGGACCCCTCGTCCACGGGGGGCAGGGGTCA

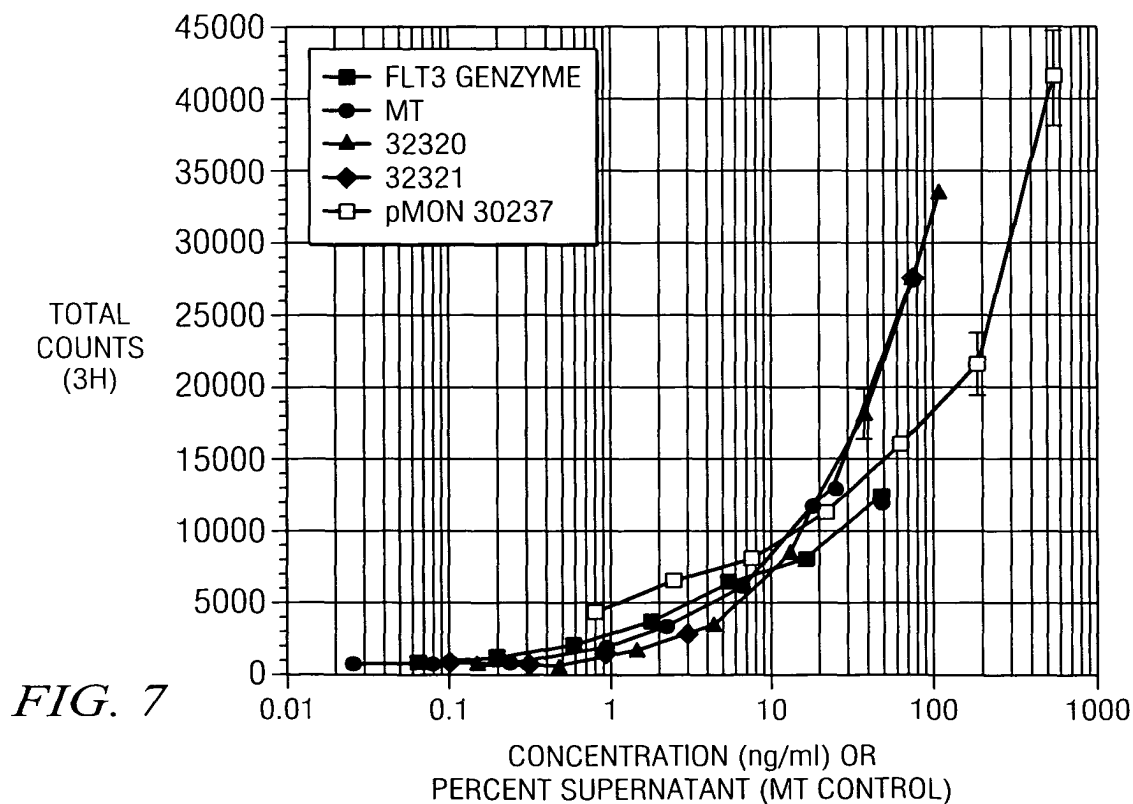
TrpGlnArgThrArgArgArgThrProArgProGlyGluGlnValProProValProSer

CCCCAGGACCTGCTGCTTGTGGAGCACTGA
601 -----+-----+-----+-----+-----+ 630
GGGGTCCTGGACGACGAACACCTCGTGACT

ProGlnAspLeuLeuLeuValGluHisEnd

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FIG. 5b



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```
ACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGT
1-----+-----+-----+-----+-----+-----+-----+ 60
TGGGTCCTGACGAGGAAGGTTGTGTGCGGGTAGAGGAGGCTGAAGCGACAGTTTTAGGCA

ThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArg

GAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGAC
61-----+-----+-----+-----+-----+-----+-----+ 120
CTCGACAGACTGATGGACGAAGTTCTAATGGGTCAGTGGCACCGGAGGTTGGACGTCCTG

GluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAsp

GAGGAGCTCTGCGGGGGCCTCTGGCGGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTC
121-----+-----+-----+-----+-----+-----+-----+ 180
CTCCTCGAGACGCCCCCGGAGACCGCCGACCAGGACCGTGTGCGGACCTACCTCGCCGAG

GluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeu

AAGACTGTGCTGCGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGGAGATACAC
181-----+-----+-----+-----+-----+-----+-----+ 240
TTCTGACAGCGACCCAGGTTCTACGTTCCGAACGACCTCGCGCACTTGTGCCTCTATGTG

LysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHis

TTTGTACCAAATGTGCCTTTCAGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAAC
241-----+-----+-----+-----+-----+-----+-----+ 300
AAACAGTGGTTTACACGGAAAGTCGGGGGGGGGTCGACAGAAGCGAAGCAGGTCTGGTTG

PheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsn

ATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACT
301-----+-----+-----+-----+-----+-----+-----+ 360
TAGAGGGCGGAGGACGTCCTCTGGAGGCTCGTCGACCACCGCGACTTCGGGACCTAGTGA

IleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThr

CGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTGAGCCC
361-----+-----+-----+-----+-----+-----+ 402
GCGGTCTTGAAGAGGGCCACGGACCTCGACGTCACAGTCGGG

ArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnPro
```

FIG. 6